IN THE CLAIMS:

Please enter the attached listing of claims into the application. This listing of claims replaces all prior listing of claims in the application.

LISTING OF CLAIMS

1. (Previously Presented) A method for promoting homologous recombination, the method comprising

generating an exogenous nucleosomal polynucleotide *in vitro* comprising:

contacting an isolated relaxed polynucleotide, the isolated polynucleotide comprising a desired sequence to be recombined, with purified histones and proteins that promote chromatin formation to generate an exogenous nucleosomal polynucleotide comprising histones;

contacting, under conditions that support homologous recombination, the exogenous nucleosomal polynucleotide with a target nucleic acid, wherein the target nucleic acid comprises a nucleotide sequence homologous to the nucleosomal polynucleotide; and

contacting the nucleosomal polynucleotide and target nucleic acid with a recombinase comprising Rad51 ~~associated~~ activity.

2-3. (Cancelled)

4. (Withdrawn) The method of claim 2, wherein the recombinase comprises Rad54 associated activity

5. (Previously Presented) The method of claim 1, wherein the recombinase is an isolated or recombinant recombinase.

6. (Withdrawn) The method of claim 2, wherein the recombinase is endogenously produced.

7. (Withdrawn) The method of claim 2, wherein the recombinase is a recombinosome.

8. (Original) The method of claim 1, wherein the contacting is *in vitro*.

9. (Withdrawn) The method of claim 1, wherein the contacting is *in vivo*.

10. (Previously Presented) The method of claim 1, wherein the target nucleic acid is an exogenously provided nucleic acid.

11. (Withdrawn) The method of claim 1, wherein the target nucleic acid sequence is an endogenous sequence.

12. (Withdrawn) The method of claim 11, wherein the endogenous sequence is a chromosomal sequence.

13. (Previously Presented) The method of claim 1, wherein the target nucleic acid comprises a coding sequence.

14. (Withdrawn) The method of claim 1, wherein the target nucleic acid sequence is non-coding sequence.

15. (Withdrawn) The method of claim 14, wherein the non-coding sequence is a promoter, enhancers, silencer, origin of replication or splicing signal sequence.

16. (Original) The method of claim 1, wherein the histones are core histones.

17. (Original) The method of claim 1, wherein the nucleosomal polynucleotide is a plasmid.

18. (Withdrawn) The method of claim 1, wherein the nucleosomal polynucleotide comprises a nucleic acid sequence that corrects a genetic mutation associated with a disease allele.

19. (Previously Presented) The method of claim 1, wherein the nucleosomal polynucleotide comprises a nucleic acid sequence that generates a genetic mutation in a targeted nucleic acid.

20. (Withdrawn) The method of claim 18, wherein the genetic mutation is selected from the group consisting of base substitutions, additions, and deletions, or any combination thereof.

21. (Previously Presented) The method of claim 19, wherein the genetic mutation alters the expression of one or more genes in a targeted nucleic acid.

22. (Withdrawn) A method of ameliorating disease caused by a disease allele, the method comprising: a) providing a nucleosomal polynucleotide comprising histones and a nucleic acid sequence that corrects a genetic mutation associated with a disease allele; and b) contacting, under conditions that support homologous recombination, the polynucleotide of a) with a target nucleic acid sequence associated with the disease allele, wherein the target nucleic acid comprises a nucleotide sequence homologous to the nucleosomal polynucleotide.

23. (Withdrawn) The method of claim 22, wherein the contacting is *in vivo*.

24. (Withdrawn) The method of claim 22, wherein the conditions that support homologous recombination include a recombinase.

25. (Withdrawn) The method of claim 24, wherein the recombinase comprises Rad51 and Rad54 associated activity.

26. (Withdrawn) The method of claim 24, wherein the recombinase is endogenously produced.

27. (Withdrawn) The method of claim 22, wherein the contacting is *in vivo*.

28. (Withdrawn) The method of claim 22, wherein the target nucleic acid sequence is an endogenous sequence.

29. (Withdrawn) The method of claim 28, wherein the endogenous sequence is a chromosomal sequence.

30. (Previously Presented) A method for promoting homologous strand pairing, the method comprising

generating an exogenous nucleosomal polynucleotide *in vitro* comprising

contacting an isolated relaxed polynucleotide, the isolated polynucleotide comprising a desired sequence to be recombined, with purified histones and proteins that promote chromatin formation to generate an exogenous nucleosomal polynucleotide comprising core histones;

contacting, under conditions that support homologous strand pairing, the exogenous nucleosomal polynucleotide with a target nucleic acid comprising a sequence homologous to the polynucleotide; and

contacting the nucleosomal polynucleotide and target nucleic acid with a recombinase comprising Rad51 activity.

31. (Previously Presented) The method of claim 19, wherein the genetic mutation is selected from the group consisting of base substitutions, additions, and deletions, or any combination thereof.

32. (Currently Amended) The method of claim 1, wherein the proteins that promote chromatin formation are selected from the group consisting of ACF, NAP1, topoisomerase I, ~~histones~~ and any combination thereof.

33. (Currently Amended) The method of claim 30, wherein the proteins that promote chromatin formation are selected from the group consisting of ACF, NAP1, topoisomerase I, ~~histones~~ and any combination thereof.